In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 25, lines 18-36 and replace it with the following paragraph:

Fig. 6

(a) Effect of increasing concentrations of RG108 on the proliferation rate of HCT116 cells. Equal amounts of cells were incubated with different concentrations of RG108 and counted after 5 days. Black bars represent results from 3 independent experiments, standard deviations are indicated by error bars. (b) Reactivation of the *p16*^{INK4a} gene (p16) in HCT116 cells treated with RG108. The upper panel shows the sequence of a wild-type RT-PCR product from cells treated with 10 μM RG108 **(SEQ ID NO: 3)**. Untreated HCT116 cells expressed only the mutant allele of *p16* (lower panel) **(SEQ ID NO: 4)**. (c) Effect of RG108 on the methylation and expression of various epigenetically silenced genes in HCT116 cells. Methylation-specific PCR (MSP) was used to analyze the methylation status of *p16*^{INK4a}, *SFRP1* and *TIMP-3* in DNA from cells incubated with 10 μM RG108. RT-PCT (RTP) was used to determine the expression level in cells incubated with 0, 10, 30 or 100 μM RG108, as indicated. β-Amyloid (βAm) was used as a loading control. (d) Effect of RG108 on the methylation status of centromeric satellite sequences. HCT116 cells were incubated with variable concentrations of RG108 (RG) or 5-azacytidine (aza), as indicated. The methylation status was analyzed by methylation-sensitive Southern analysis. The size of marker fragments (in kbp) is indicated on the sides of the panels, respectively.

pop.doub. after 5d, number of the cell population doublings after 5 days; ctrl., control; α-sat., α-satellite; sat. 2, satellite 2.

Please delete the paragraph on page 32, lines 5-16 and replace it with the following paragraph:

Example 12

Bisulfite sequencing was performed under standard conditions (Frommer, M., et al., 1992. A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in

individual DNA strands. Proc. Natl. Acad. Sci. USA, 89: 1827-1831) with genomic DNA from HCT116 cells treated with 30 μM RG108 or no inhibitor for 5 days. The primers used and the PCR conditions were as follows: forward TTTGTTTTTTTAGTTTTTGTTTTTT **(SEQ ID NO: 1)**, reverse AATCCCCCAAACTCCAACTAC **(SEQ ID NO: 2)**, 95 °C 3 min., 38 cylces (95 °C 30 s, 58 °C 30 s, 72 °C 30 s), 72 °C 5 min. PCR products were purified using the QIAquick Gel Extraction Kit (Qiagen), subcloned into the pCR 4-Topo plasmid vector (Invitrogen) and subjected to automated sequencing. The results are shown in Fig. 7. The analysis revealed significant demethylation of the CpG dinucleotides of the TIMP-3 CpG island in RG108 treated cells ($P < 0.05$, as determined by a t-test).